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TECH CENTER 1600/2900

- 1 -

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<140> US 09/691,763

<141> 2000-10-18

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2821

<212> DNA

<213> Homo Sapiens

<400> 1

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ccacacacag	ctatttccag	gtacattctt	gacgctagga	attcagcaaa	gaataagaca	300
gttaaggtct	ccgatgctca	taggcctcac	attttagaga	gggatgaatg	tccaataagc	360
atataaacat	ataatatgtc	agggtcgtat	gactacaagg	aacagtgatt	gttacaaccc	420
agatgagagg	gaaaaataaa	ggattccaaa	tatccccctt	gggaagtaga	gtcaggattc	480
aaacaaagaa	ctgtatggct	tcaagttcat	ggtctttaat	ctcctggagg	ctgtctctct	540
ttcttttttc	ttttttttaa	tcagtgttgg	gatcaaattc	tggctccctt	aggaagcatc	600
tggcaagggt	tcgggagcca	tcgggttggc	catgttatgc	tggaatattt	ataagcaccg	660
gagggttatc	cccatgtcgt	agaaaatgaa	actgaagctc	agagagattt	gcactctctg	720
cccttttgta	caactcattt	ttccccagta	tgtggaattg	aggagacttc	acgcttctag	780
ctgtcatgat	tccaagattc	tacgacatgt	gggagaggat	cctaaggttc	ggggaaccgc	840
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gagagccagc	ccaggtttcc	ggtctgtacc	cgctgggtgc	agcccagaga	caagcaggcg	960
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tgaggcctcc	acacccagcc	cggccccacc	gcactcctgc	acagcctgca	tctgtgctcc	1860
cgcaaccagg	gcagggcagg	gcagggcagg	caaggcttgg	caaccctgcg	cacccacccc	1920
accaacccac	accctgcggg	ggaagggaga	caatattacc	ctcatcccac	tgcattgtgg	1980
gtcctggtgg	ccgccccctg	gagccctgcc	cctaggcttg	cagaggaatt	cctgaagaac	2040

83

C

tcaagttcag	cagggacag	ccccacaccc	tggtgctg	ctcatgttct	cctcccaccc	2100
ccaggcctgc	actttataga	ccagcacccg	gctgcgctta	tcgcgaggg	cacaaacgtt	2160
gagtggctgc	tggtatgctct	gtacgggaag	gtcctgacgg	atgagcagta	ccaggcagtg	2220
cgggccgagc	ccaccaaccc	aagcaagatg	cggagctct	tcagtttcac	accagcctgg	2280
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gccacccagc	ctccagctcc	atgtccctag	ggctctctgg	accccaa	cttcccccat	2580
ccttcctggt	atcgccatgg	aatatccctc	ctcattcacc	aggtggtgct	cctccagtg	2640
tccctaaagg	gtctaaccct	accattatag	ataacagcct	gtgaccagg	tccgaaggtt	2700
aaaagaggca	tgtaccaaag	ggcgcaaa	ggtgggcagc	tctgtccaag	ccatttagaa	2760
acacactagt	cttcatagct	cccctacctt	ccacattttc	caactggaaga	aaaaatggca	2820
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 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (75)...(662)

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	Met Gly	Arg Ala	Arg Asp	Ala Ile	Leu Asp	
	1		5		10	
gag aac	ctg acc	gcc gag	gag ctc	aag aag	ttc aag	158
Glu Asn	Leu Thr	Ala Glu	Glu Leu	Lys Lys	Phe Lys	
	15		20		25	
tcg gtg	ccg ctg	cgc gag	ggc tac	ggg cgc	atc ccg	206
Ser Val	Pro Leu	Arg Glu	Gly Tyr	Gly Arg	Ile Pro	
	30		35		40	
ctg tcc	atg gac	gcc ttg	gac ctc	acc gac	aag ctg	254
Leu Ser	Met Asp	Ala Leu	Asp Leu	Thr Asp	Lys Leu	
	45		50		55	
ctg gag	acc tac	ggc gcc	gag ctc	acc gct	aac gtg	302
Leu Glu	Thr Tyr	Gly Ala	Glu Leu	Thr Ala	Asn Val	
		65		70		
ggc ctg	cag gag	atg gcc	ggg cag	ctg cag	gcg gcc	350
Gly Leu	Gln Glu	Met Ala	Gly Gln	Leu Gln	Ala Ala	
	80			85		
tct gga	gcc gcg	cca gct	ggg atc	cag gcc	cct cct	398
Ser Gly	Ala Ala	Pro Ala	Gly Ile	Gln Ala	Pro Pro	
	95		100		105	
aag cca	ggc ctg	cac ttt	ata gac	cag cac	cg	446
Lys Pro	Gly Leu	His Phe	Ile Asp	Gln His	Arg Ala	
	110		115		120	
agg gtc	aca aac	gtt gag	tgg ctg	ctg gat	gct ctg	494
Arg Val	Thr Asn	Val Glu	Trp Leu	Leu Asp	Ala Leu	

125	130	135	140	
ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca				542
Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro				
145	150	155		
agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc				590
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr				
160	165	170		
tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg				638
Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu				
175	180	185		
gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc				692
Val Glu Asp Leu Glu Arg Ser *				
190	195			
cctggcaatc ccaccaaatc atcctgaatc tgatcttttt atacacaata tacgaaaagc				752
cagcttgaaa aaaaaaaaa				770

<210> 3
 <211> 195
 <212> PRT
 <213> Homo Sapiens

<400> 3

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1	5	10	15	
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu				
20	25	30		
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp				
35	40	45		
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr				
50	55	60		
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu				
65	70	75	80	
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala				
85	90	95		
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu				
100	105	110		
His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn				
115	120	125		
Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu				
130	135	140		
Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg				
145	150	155	160	
Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu				
165	170	175		
Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu				
180	185	190		
Glu Arg Ser				
195				

<210> 4
 <211> 626
 <212> DNA
 <213> Homo Sapiens

<400> 4

ES

C

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gggtgagcgg cggcagcggc cggggatcct ggagccatgg ggcgcgcgcg cgacgccatc 180
ctggatgcgc tggagaacct gaccgccgag gagtcaaga agttcaagct gaagctgctg 240
tcggtgccgc tgcgcgaggg ctacgggcgc atcccgcggg gcgcgctgct gtccatggac 300
gccttggacc tcaccgacaa gctggtcagc ttctacctgg agacctacgg cgccgagctc 360
accgctaacg tgctgcgcga catgggcctg caggagatgg ccgggcagct gcaggcggcc 420
acgcaccagg gtgagccgcc cccgttcccc tccaccccg tttcccctc caccacacc 480
agcgttacc ccgcgggctc ttccgcttcc tgttcctcct acccctaaac aaagctgctc 540
taccggaaag gaggtcctcc acgcttggcc taccgaccaa cgggaccccc gccccacggc 600
gggaaggga ggaaggga tcactt 626

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<211> 340
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (67)...(339)

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ggagcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg gag aac 108
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
1 5 10

ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg 156
Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
15 20 25 30

ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc 204
Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
35 40 45

atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag 252
Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
50 55 60

acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg 300
Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
65 70 75

cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g 340
Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
80 85 90

<210> 6
<211> 91
<212> PRT
<213> Homo Sapiens

<400> 6
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45

Ed

C

Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
 50 55 60
 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
 65 70 75 80
 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
 85 90

<210> 7
 <211> 57
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (3)...(56)

<400> 7
 gc tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca 47
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
 1 5 10 15

gcc aag cca g 57
 Ala Lys Pro

<210> 8
 <211> 18
 <212> PRT
 <213> Homo Sapiens

<400> 8
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
 1 5 10 15
 Lys Pro

<210> 9
 <211> 356
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (3)...(258)

<400> 9
 gc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc 47
 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val
 1 5 10 15

aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg 95
 Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr
 20 25 30

gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag 143
 Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys
 35 40 45

atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag 191

87

03

Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys
50 55 60

gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag 239
Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu
65 70 75

gac ctg gag cgg agc tga g gctccttccc agcaacactc cggtcagccc 288
Asp Leu Glu Arg Ser *
80

ctggcaatcc caccaaata tccatgaatct gatcttttta tacacaatat acgaaaagcc 348
agcttgaa 356

<210> 10
<211> 84
<212> PRT
<213> Homo Sapiens

<400> 10
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
1 5 10 15
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
20 25 30
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
35 40 45
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
50 55 60
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
65 70 75 80
Leu Glu Arg Ser

<210> 11
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 11
gcactttata gaccagca 18

<210> 12
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 12
atttggtggg attgccag 18

<210> 13
<211> 17
<212> DNA
<213> Homo Sapiens

<400> 13
tgggcctgca ggagatg 17

<210> 14
<211> 22
<212> DNA

BB

C

<213> Homo Sapiens

<400> 14
ccttcctggg catggagtcc tg 22

<210> 15
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 15
ggagcaatga tcttgatctt c 21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 16
ggttgtagtg gggtagtg t 21

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 17
caaaacatcc ataaacaaca acaca 25

<210> 18
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 18
ttgtagcggg gtgagcggc 19

<210> 19
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 19
aacgtccata aacaacaacg cg 22

<210> 20
<211> 803
<212> DNA
<213> Mus Musculus

<220>
<221> CDS
<222> (162)...(743)

89

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 aagcagctga cttcctgggc ttggcgggct ggcagcaggc aggcctgagca ggcgagcagc 120
 agcaagagta aaaggtgacc gcggctgccc accccagagc c atg ggg cgg gca cga 176
 Met Gly Arg Ala Arg
 1 5

gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa 224
 Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys
 10 15 20

aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg 272
 Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly
 25 30 35

cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act 320
 Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr
 40 45 50

gac aaa ctt gtc agc tac tat ctg gag tgc tat ggc ttg gag ctc aca 368
 Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr
 55 60 65

atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg 416
 Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu
 70 75 80 85

caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc 464
 Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ser Val
 90 95 100

cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg 512
 Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg
 105 110 115

caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct 560
 Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala
 120 125 130

ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca 608
 Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala
 135 140 145

gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca 656
 Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro
 150 155 160 165

tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa 704
 Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu
 170 175 180

ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatctttt 753
 Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *
 185 190

ccagctacat tatctagctc ctgactttgt atacacaatt ttgaaaaaa 803

<210> 21
 <211> 193
 <212> PRT

gc

C

<213> Mus Musculus

<400> 21

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser
1 5 10 15
Gly Asp Glu Leu Lys Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp
35 40 45
Ala Ile Asp Leu Thr Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr
50 55 60
Gly Leu Glu Leu Thr Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Leu Ala Glu Gln Leu Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala
85 90 95
Ala Ala Ala Ser Val Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe
100 105 110
Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp
115 120 125
Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr
130 135 140
Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu
145 150 155 160
Phe Ser Phe Val Pro Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu
165 170 175
Gln Ala Leu Lys Glu Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln
180 185 190
Ser

<210> 22

<211> 605

<212> DNA

<213> Rattus Norvegicus

<220>

<221> CDS

<222> (2)...(518)

<220>

<221> Variant

<222> (109)...(109)

<223> y = C or T/U

<400> 22

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Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
1 5 10 15
atc cca cgg ggg gcc ctg ctg cag atg gac ccc ata gac ctc act gat 97
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30
aaa ctc gtc agy tac tat ctg gag ggg tat ggc ttg gag ctc aca atg 145
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45
act gtg ctt aga gac atg ggc ata cag gag ctg gct gag cag ctg caa 193

Thr	Val	Leu	Arg	Asp	Met	Gly	Ile	Gln	Glu	Leu	Ala	Glu	Gln	Leu	Gln		
50						55					60						
aag	att	atg	gaa	gag	tct	gga	gct	gtg	gct	act	gca	acc	agt	gtc	cct	241	
Lys	Ile	Met	Glu	Glu	Ser	Gly	Ala	Val	Ala	Thr	Ala	Thr	Ser	Val	Pro		
65					70				75						80		
gct	cag	ggc	aca	gcc	aga	aca	gaa	cat	ttt	gtg	gac	caa	cac	agg	caa	289	
Ala	Gln	Gly	Thr	Ala	Arg	Thr	Glu	His	Phe	Val	Asp	Gln	His	Arg	Gln		
				85					90					95			
gca	ctc	att	gcc	agg	gtc	aca	gaa	gtt	gat	ggg	ttg	ctg	gat	gct	ctg	337	
Ala	Leu	Ile	Ala	Arg	Val	Thr	Glu	Val	Asp	Gly	Leu	Leu	Asp	Ala	Leu		
			100					105					110				
tat	ggc	aat	gtg	ctg	act	gaa	gga	cag	tac	cag	gca	gtt	cgt	gca	gag	385	
Tyr	Gly	Asn	Val	Leu	Thr	Glu	Gly	Gln	Tyr	Gln	Ala	Val	Arg	Ala	Glu		
	115						120					125					
acc	acc	aac	caa	aac	aag	atg	agg	aag	ctc	ttt	agc	ttt	gct	cca	gcc	433	
Thr	Thr	Asn	Gln	Asn	Lys	Met	Arg	Lys	Leu	Phe	Ser	Phe	Ala	Pro	Ala		
	130					135					140						
tgg	aac	ctg	acc	tgc	aag	aac	ttg	ttc	ctt	gag	gcc	ttg	agg	caa	aca	481	
Trp	Asn	Leu	Thr	Cys	Lys	Asn	Leu	Phe	Leu	Glu	Ala	Leu	Arg	Gln	Thr		
145					150					155					160		
cag	ccc	tac	ttg	gtg	aca	gac	ctg	gaa	cag	agc	tga	g	gtatcttttc			528	
Gln	Pro	Tyr	Leu	Val	Thr	Asp	Leu	Glu	Gln	Ser	*						
			165						170								
cagctacaca	tctagctcct	ggttttgtat	acaaaatttt	ctaaaaacaa	gtttgtattt	588											
gtgttttctc	gaaaaaa					605											

<210> 23
 <211> 171
 <212> PRT
 <213> Rattus Norvegicus

 <220>
 <221> Unknown
 <222> (36)...(36)
 <223> Xaa can be any amino acid.

<400> 23
 Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
 1 5 10 15
 Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
 20 25 30
 Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
 35 40 45
 Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
 50 55 60
 Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
 65 70 75 80
 Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
 85 90 95
 Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
 100 105 110
 Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu

115	120	125
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala		
130	135	140
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr		
145	150	155
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser		160
	165	170

<210> 24
 <211> 713
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (75)...(605)

<400> 24

ccacgcgtcc gacttctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg 60
 gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
 1 5 10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
 Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
 15 20 25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
 Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
 30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
 45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
 65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
 Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
 80 85 90

ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca 398
 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
 95 100 105

aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat 446
 Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
 110 115 120

gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg 494
 Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
 125 130 135 140

cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac 542
 Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
 145 150 155

ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac 590

9.3

03

Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
160 165 170

ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc cctggcaatc 645
Leu Glu Arg Ser *
175

ccaccaaata atcctgaata tgatcttttt atacacaata tacgaaaagc cagcttgaaa 705
aaaaaaaa 713

<210> 25
<211> 176
<212> PRT
<213> Homo Sapiens

<400> 25
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Leu His Phe Ile
85 90 95
Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp
100 105 110
Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln
115 120 125
Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg Lys Leu Phe
130 135 140
Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu Leu Leu Gln
145 150 155 160
Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu Glu Arg Ser
165 170 175

<210> 26
<211> 405
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (75)...(404)

<400> 26
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gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10
gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
15 20 25
tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu

94

C

30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
 45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
 65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
 Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
 80 85 90

tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
 95 100 105

aag cca g 405
 Lys Pro
 110

<210> 27
 <211> 110
 <212> PRT
 <213> Homo Sapiens

<400> 27

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
 1 5 10 15
 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
 20 25 30
 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
 35 40 45
 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
 50 55 60
 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
 65 70 75 80
 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
 85 90 95
 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro
 100 105 110

95

1